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FIGURE 1A

1 GCACGAGAACTTTGCTGTGCGCGTTCTCCCGCGCGGGCTCAACTTTGTAGAGCGAGG 60  
61 GGCCAACTTGGCAGAGCGCGCGCCAGCTTTGCAGAGAGCGCCCTCCAGGGACTATGCGT 120  
121 GCGGGGACACGGGTGCGTTTGGGCTCTTCCACCCCTGCGGAGCGCACTACCCGAGCCAG 180  
181 GGGCGGTGCAAGCCCCGCCCGGCCCTACCCAGGGGGCTCCTCCCTCCGAGCGCCGAGA 240  
241 CTTTTAGTTTCGCTTTTCGCTAAAGGGGCCCCAGACCCTTGCTGCGGAGCGACGGAGAGAG 300  
301 ACTGTGCCAGTCCCAGCGCCCTACCGCGTGGGAACGATGGCAGATGATCAGGGCTGTA 360  
1 M A D D Q G C I 8  
361 TTGAAGAGCAGGGGGTTGAGGATTTCAGCAAATGAAGATTTCAGTGGATGCTAAGCCAGACC 420  
9 E E Q G V E D S A N E D S V D A K P D R 28  
421 GGTCTCGTTTGTACCGTCCCTCTTCAGTAAGAAGAAGAAAATGTCACCATGCGATCCA 480  
29 S S F V P S L F S K K K K N V T M R S I 48  
481 TCAAGACCACCGGGACCGAGTGCCTACATATCAGTACAACATGAATTTTGAAAAGCTGG 540  
49 K T T R D R V P T Y Q Y N M N F E K L G 68  
541 GCAAATGCATCATAATAACAACAAGAAGCTTTGATAAAGTGACAGGTATGGGCGTTCGAA 600  
69 K C I I I N N K N F D K V T G M G V R N 88  
601 ACGGAACAGACAAAGATGCCGAGGCGCTCTTCAAGTGCTTCCGAAGCCTGGGTTTGTACG 660  
89 G T D K D A E A L F K C F R S L G F D V 108  
661 TGATTGTCTATAATGACTGCTCTTGTGCCAAGATGCAAGATCTGCTTAAAAAAGCTTCTG 720  
109 I V Y N D C S C A K M Q D L L K K A S E 128  
721 AAGAGGACCATACAAATGCCGCTGCTTGCCTGCATCCTCTTAAGCCATGGAGAAGAAA 780  
129 E D H T N A A C F A C I L L S H G E E N 148  
781 ATGTAATTTATGGGAAAGATGGTGTACACCAATAAAGGATTTGACAGCCCACTTTAGGG 840  
149 V I Y G K D G V T P I K D L T A H F R G 168  
841 GGGATAGATGCAAAACCCCTTTTAGAGAAACCCAAACTCTTCTTCATTTCAGGCTTGCCGAG 900  
169 D R C K T L L E K P K L F F I Q A C R G 188  
901 GGACCGAGCTTGATGATGCCATCCAGGCCGACTCGGGGCCCCATCAATGACACAGATGCTA 960  
189 T E L D D A I Q A D S G P I N D T D A N 208

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FIGURE 1B

961	ATCCTCGATACAAGATCCCAGTGGAGCTGACTTCCTCTTCGCCTATTCCACGGTTCCAG	1020
209	P R Y K I P V E A D F L F A Y S T V P G	228
1021	GCTATTACTCGTGGAGGAGCCCAGGAAGAGGCTCCTGGTTGTGCAAGCCCTCTGCTCCA	1080
229	Y Y S W R S P G R G S W F V Q A L C S I	248
1081	TCCTGGAGGAGCACGGAAAAGACCTGGAAATCATGCAGATCCTCACCAGGGTGAATGACA	1140
249	L E E H G K D L E I M Q I L T R V N D R	268
1141	GAGTTGCCAGGCACCTTTGAGTCTCAGTCTGATGACCCACACTTCCATGAGAAGAAGCAGA	1200
269	V A R H F E S Q S D D P H F H E K K Q I	288
1201	TCCCTGTGTGGTCTCCATGCTCACCAAGGAACCTCTACTTCAGTCAATAGCCATATCAGG	1260
289	P C V V S M L T K E L Y F S Q	303
1261	GGTACATTCTAGCTGAGAAGCAATGGGTCACTCATTAAATGAATCACATTTTTTTATGCTC	1320
1321	TTGAAATATTTCAGAAATTCTCCAGGATTTTAATTTTCAGGAAAATGTATT	1369

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FIGURE 2A

1 GCACGAGCGGATGGGTGCTATTGTGAGGCGGTTGTAGAAGAGTTTCGTGAGTGCTCGCAG 60  
61 CTCATACCTGTGGCTGTGTATCCGTGGCCACAGCTGGTTGGCGTCGCCCTGAAATCCCAG 120  
121 GCCGTGAGGAGTTAGCGAGCCCTGCTCACACTCGGCGCTCTGGTTTTCGGTGGGTGTGCC 180  
181 CTGCACCTGCCTCTTCCCGCATTCTCATTAAATAAAGGTATCCATGGAGAACACTGAAAAC 240  
1 M E N T E N 6  
241 TCAGTGGATTCAAAATCCATTAAAAATTTGGAACCAAAGATCATACTGGAAGCGAATCA 300  
7 S V D S K S I K N L E P K I I H G S E S 26  
301 ATGGACTCTGGAATATCCCTGGACAACAGTTATAAAATGGATTATCCTGAGATGGGTTTA 360  
27 M D S G I S L D N S Y K M D Y P E M G L 46  
361 TGTATAATAATTAATAATAAGAATTTTCATAAAAGCACTGGAATGACATCTCGGTCTGGT 420  
47 C I I I N N K N F H K S T G M T S R S G 66  
421 ACAGATGTGATGCAGCAAACCTCAGGGAAACATTGAGAACTTGAAATATGAAGTCAGG 480  
67 T D V D A A N L R E T F R N L K Y E V R 86  
481 AATAAAAATGATCTTACACGTGAAGAAATTGTGGAATTGATGCGTGATGTTTCTAAAGAA 540  
87 N K N D L T R E E I V E L M R D V S K E 106  
541 GATCACAGCAAAGGAGCAGTTTTGTTTGTGTGCTTCTGAGCCATGGTGAAGAAGGAATA 600  
107 D H S K R S S F V C V L L S H G E E G I 126  
601 ATTTTGGAAACAAATGGACCTGTTGACCTGAAAAAATAACAACTTTTTCAGAGGGGAT 660  
127 I F G T N G P V D L K K I T N F F R G D 146  
661 CGTTGTAGAAGTCTAACTGGAACCCAACTTTTCATTATTCAGGCCTGCCGTGGTACA 720  
147 R C R S L T G K P K L F I I Q A C R G T 166  
721 GAACTGGACTGTGGCATTGAGACAGACAGTGGTGTGATGATGACATGGCGTGTCATAAA 780  
167 E L D C G I E T D S G V D D D M A C H K 186  
781 ATACCAGTGGAGGCCGACTTCTGTATGCATACTCCACAGCACCTGGTTATTATTCTTGG 840  
187 I P V E A D F L Y A Y S T A P G Y Y S W 206

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FIGURE 2B

841 CGAAATTCAAAGGATGGCTCCTGGTTCATCCAGTCGCTTTGTGCCATGCTGAAACAGTAT 900  
207 R N S K D G S W F I Q S L C A M L K Q Y 226

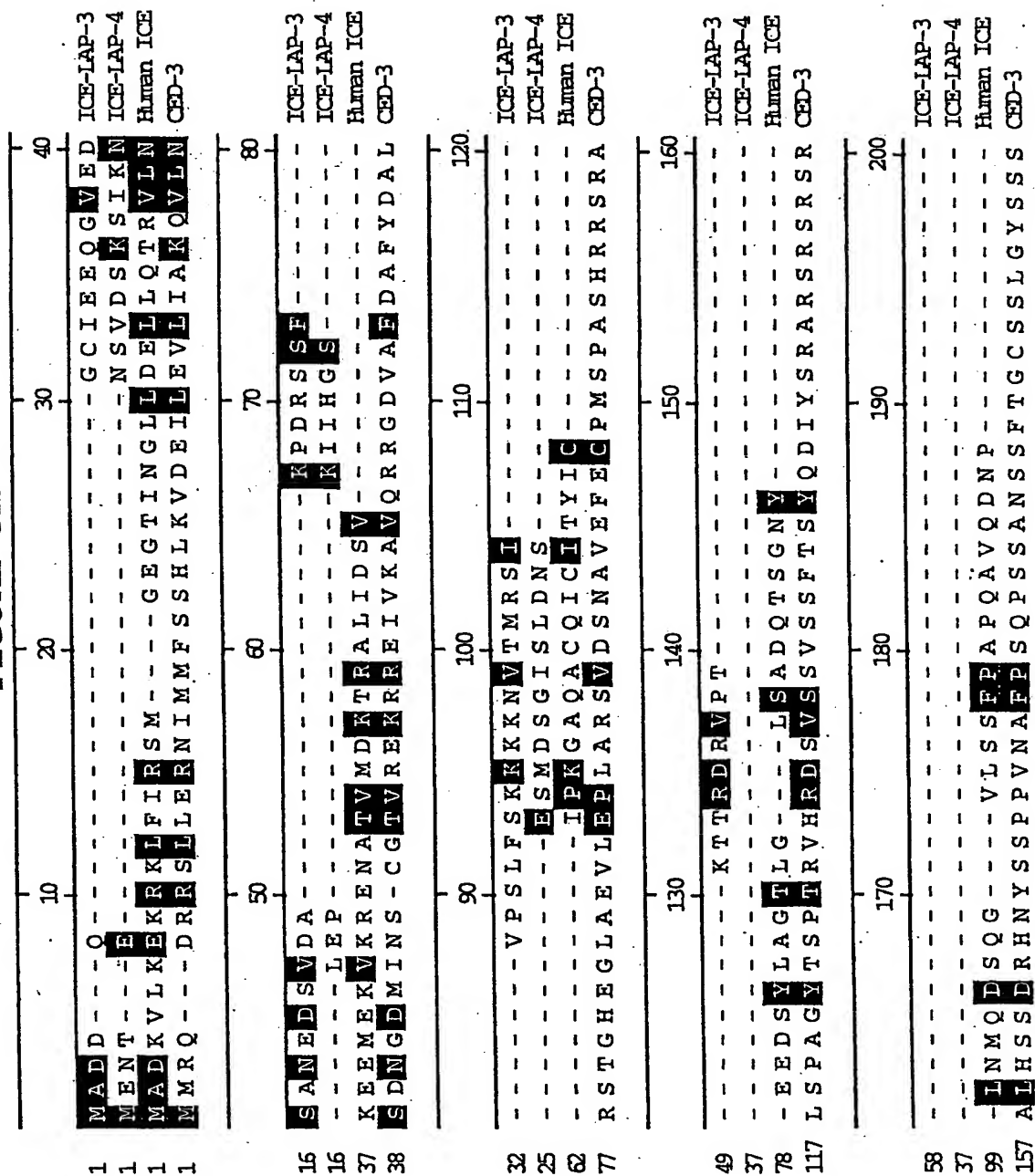
901 GCCGACAAGCTTGAATTTATGCACATTCTTACCCGGGTTAACCGAAAGGTGGCAACAGAA 960  
227 A D K L E F M H I L T R V N R K V A T E 246

961 TTTGAGTCCTTTTCCTTTGACGCTACTTTTCATGCAAAGAAACAGATTCCATGTATTGTT 1020  
247 F E S F S F D A T F H A K K Q I P C I V 266

1021 TCCATGCTCACAAAAGAACTCTATTTTTATCACTAAAGAAATGGTTGGTTGGTGGTTTTT 1080  
267 S M L T K E L Y F Y H \* 277

1081 TTTAGTTTGTATGCCAAGTGAGAAGATGGTATATTTGGGTACTGTATTTCCCTCTCATTG 1140

1141 GGGACCTACTCTCATGCTG 1159



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FIGURE 3B

	210	220	230	240	
58	---	YQYN	MNFEKL	---	ICE-LAP-3
37	---	YK	MDYPEM	---	ICE-LAP-4
122	AMP	TS	SGS	---	Human ICE
197	RNR	SF	SKASG	PTQY	CED-3
	250	260	270	280	
68	---	GKCI	IINN	KNF	ICE-LAP-3
45	---	GLCI	IINN	KNF	ICE-LAP-4
153	YPI	MDK	SSR	TR	Human ICE
235	YRNF	SS	PRGM	CL	CED-3
	290	300	310	320	
98	FKCF	RLG	FD	VI	ICE-LAP-3
75	RETF	RNL	KYE	VR	ICE-LAP-4
190	TML	QNL	GY	SV	Human ICE
270	TNLF	RCMG	YTV	ICK	CED-3
	330	340	350	360	
136	CFAC	IL	LSHG	EE	ICE-LAP-3
113	SFVC	VLL	SHG	EE	ICE-LAP-4
230	TFL	VFM	SHG	IRE	Human ICE
308	AIL	VIL	SHG	EE	CED-3
	370	380	390	400	
170	RCK	TL	LEK	PK	ICE-LAP-3
147	RCR	SL	TGK	PK	ICE-LAP-4
269	NCP	SL	KDK	PK	Human ICE
342	NAP	RL	ANK	PK	CED-3

**FIGURE 3C**

[illegible]

Decoration 'Decoration #1': Shade (with solid black) residues that match the Consensus exactly.